

# STIC EIC 2100 Search Request Form

146689

Today's Date:

03/03/05

What date would you like to use to limit the search?

Priority Date: 07/19/2001 Other:

Name

JD, BBO200C

AU

2162

Examiner #

78889

Room #

3B31

Phone

24041

Serial #

09/682 050

Format for Search Results (Circle One):

PAPER

DISK

EMAIL

Where have you searched so far?

USP

DWPI

EPO

JPO

ACM

IBM

TDB

IEEE

INSPEC

SPI

Other

Is this a "Fast & Focused" Search Request? (Circle One) YES NO

A "Fast & Focused" Search is completed in 2-3 hours (maximum). The search must be on a very specific topic and meet certain criteria. The criteria are posted in EIC2100 and on the EIC2100 NPL Web Page at <http://ptoweb/patents/stic/stic-tc2100.htm>.

What is the topic, novelty, motivation, utility, or other specific details defining the desired focus of this search? Please include the concepts, synonyms, keywords, acronyms, definitions, strategies, and anything else that helps to describe the topic. Please attach a copy of the abstract, background, brief summary, pertinent claims and any citations of relevant art you have found.

experiment templates, table, form spreadsheet  
inby identify with attributes

STIC Searcher

Geoffrey St. Leger

Phone

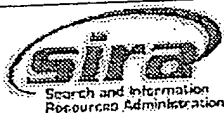
23540

Date picked up

3/3/5

Date Completed

3/3/5





# STIC Search Report

## EIC 2100

STIC Database Tracking Number: 146689

TO: Baoquoc To  
Location: RND 3B31  
Art Unit : 2162  
Thursday, March 03, 2005

Case Serial Number: 09/682098

From: Geoffrey St. Leger  
Location: EIC 2100  
Randolph-4B31  
Phone: 23450

geoffrey.stleger@uspto.gov

### Search Notes

Dear Examiner To,

Attached please find the results of your search request for application 09/682098. I searched Dialog's patent files, technical databases and general files; along with the Internet.

Please let me know if you have any questions.

Regards,



Geoffrey St. Leger  
4B30/308-7800

[CrossFire 2000](#)

[Dr. Heller Joins MDL](#)

[Beilstein and MDL](#)

[Assay Explorer 1.1](#)

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**MDL RELEASES ASSAY EXPLORER 1.1,  
ITS BIOLOGICAL DATA MANAGEMENT  
SYSTEM WITH INTEGRATED  
MICROSOFT VBA**

**—With VBA, MDL Customers Can Integrate  
Applications, and Customize and Extend Assay  
Explorer to Help Biologists Capture, Analyze, Report,  
and Manage All Their Biological Data—**

SAN LEANDRO, California—**June 9, 2000**—MDL Information Systems, Inc., the recognized leader in discovery informatics for the life science and chemical industries, announced the release of Assay Explorer 1.1, MDL's flexible and extensible biological information management system. Assay Explorer 1.1 is the first MDL product to integrate Microsoft Visual Basic for Applications (VBA). Designed for biologists, Assay Explorer is the only commercially available system that enables them to define and capture all of their experimental results and methodology.

Dr. John Burns, manager of Assay Explorer development at MDL, states "The integration of Microsoft VBA into Assay Explorer provides our customers with the industry standard in application development. Using familiar tools, developers can customize, integrate other VBA applications, and enhance the functionality of Assay Explorer."

Assay Explorer's user interface is simple and easy to use, allowing scientists to very quickly become productive

without tedious template design. A separate administration module provides tools for administrators to easily control features such as dictionaries, variables, result mapping, and linked database tables. Some key features of Assay Explorer 1.1 are

- Open API (Application Programming Interface) to all Assay Explorer objects, including tables and charts, through Microsoft VBA development environment
- Industry standard ISIS/Object Library for retrieval and display of chemical structures from ISIS databases
- Customizable protocol and experiment templates that place no limits on experimental variables or conditions
- Flexible result mapping tools that let administrators manage mapping to an extensible data model
- User friendly UIs for both basic and advanced experiment creation that free researchers and administrators from managing complex data input templates

"We are delighted that MDL has integrated VBA into its biological information management system, Assay Explorer," said Microsoft VBA Group Product Manager Neil Charney. "VBA will enable MDL's customers to customize Assay Explorer's user interface and easily integrate with other VBA-enabled applications to provide a complete biological data management solution. The combination of Assay Explorer's exposed API and VBA customization allows developers to meet the needs of all biologists for a truly integrated corporate data management solution."

Assay Explorer is a fully featured, out-of-the-box application, and its exposed API and integrated Microsoft VBA engine enable developers to easily customize and extend its functionality. VBA add-ins can be easily created to add functionality to the Assay Explorer client application. Furthermore, add-ins can be configured to deliver only to designated scientists for each task, thereby providing greater control over application security. Other possible extensions include:

- Custom functions to call out to external calculation engines for complex statistical analysis
- Assay Explorer protocol and experiment document links to existing reporting mechanisms
- Validation routines during data entry or before storage to Oracle databases
- Custom data entry UIs for *in vivo*, agrochemical, or other experiments

## About MDL

MDL Information Systems ("MDL") is the recognized leader in discovery informatics for the life science and chemical industries. MDL software, content, and services provide the enterprise framework for identifying successful new products. MDL is an international business headquartered in San Leandro, CA with offices worldwide. MDL Information Systems, Inc. is a wholly owned subsidiary of Elsevier Science, Inc.

CONTACT: Marketing Communications  
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(510) 357-2222, ext. 1477  
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# Realizing the Benefits



## Assay Explorer

**M**anaging biological information has been an intractable problem for many research organizations. The trouble comes with trying to manage the complexity of the data now generated routinely by modern labs while still providing a system that is easy for scientists to use and for IT to update. Can you have your cake and eat it too?

The answer today is a resounding "Yes," thanks to Assay Explorer, MDL's newest solution for biological information management. For Assay Explorer is the only commercial system that combines both the tools for capturing and analyzing experimental results with an underlying platform that can, indeed, handle all of the different experimental data types that might interest biologists now and in the future.

"The key to Assay Explorer is its built-in flexibility," explained Ron Delmendo, product manager of biology products at MDL. The components used to develop the application evolved directly from MDL's experiences producing the Life Science Workbench toolboxes. Assay Explorer, however, is a full-fledged end-user application, designed to be used out of the box. Biologists can quickly and easily define even the most complex experiments without relying on difficult-to-maintain templates. And flexible results displays enable them to see the data in the way that makes the most sense to them.

"Adding a new reader or changing an experimental setup shouldn't require scientists or IT groups to create entirely new applications from scratch," Delmendo stated.

### The Importance of Being Extensible

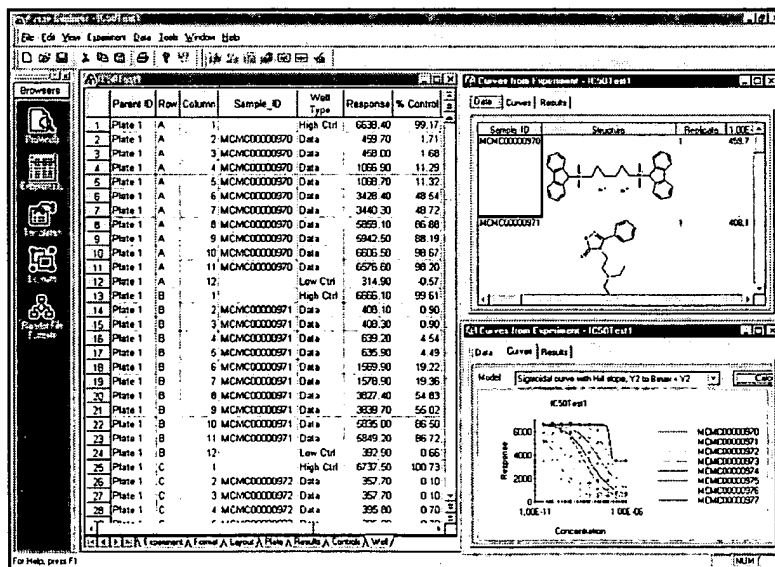
Extensibility is more system requirement than buzzword for life science labs. New technologies in assay design, experimental procedures, and laboratory automation continue to revolutionize the way biologists work. Simultaneously, global research efforts like the Human Genome Project are giving

scientists a better understanding of the molecular basis for biological activity. Discoveries are waiting to be made—but making them demands an intuitive way to capture, analyze, report, and manage different types of data from disparate sources.

"With all of the data that biologists now need to access, tools like Microsoft Excel just can't keep up," Delmendo commented. Loading data into Excel often requires a tremendous amount of cutting and pasting to associate the right results with the right sample, concentration, or other variable. Custom macros can help, but according to Delmendo, scientists then spend their time creating macros. "If you change your setup, or if the manufacturer changes the software, you have to write another macro," Delmendo said. "Basically, you spend too much time programming, and that slows down your research."

**"The integrated VB API ensure that today's scientists can embrace the new and assay technology."**

*Dr. John Burns, Assay Explorer Project*



Assay Explorer's decision interface offers scientists several ways to view data. In this example, scientists are looking at raw data, calculated results, IC<sub>50</sub> curves, and associated chemical structures. Data can be sorted and filtered by any criteria and exported for retest or follow-up studies.



# of Built-in Flexibility

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ay's life science labs  
ewest automation  
ologies quickly."**

Leader, MDL Information Systems, Inc.

IT groups, too, find it challenging to keep up with changes in the way biological data is managed and communicated. In current systems, each change in assay design or results measurement requires IT staff to change the user interface, the underlying data model, or both. Scientists must either wait for the changes to be implemented before running their experiments, or run the experiment using less than adequate tools that can capture only a portion of the results.

Assay Explorer offers a commercial solution with the extensibility needed to manage the complexity of the data generated by today's research methods. "Two basic credos guide Assay Explorer design," said Dr. John Burns, Assay Explorer project leader at MDL. "First, scientists should never have to wait for IT before running an experiment. Second, all relevant data must be stored in the system for retrieval later."

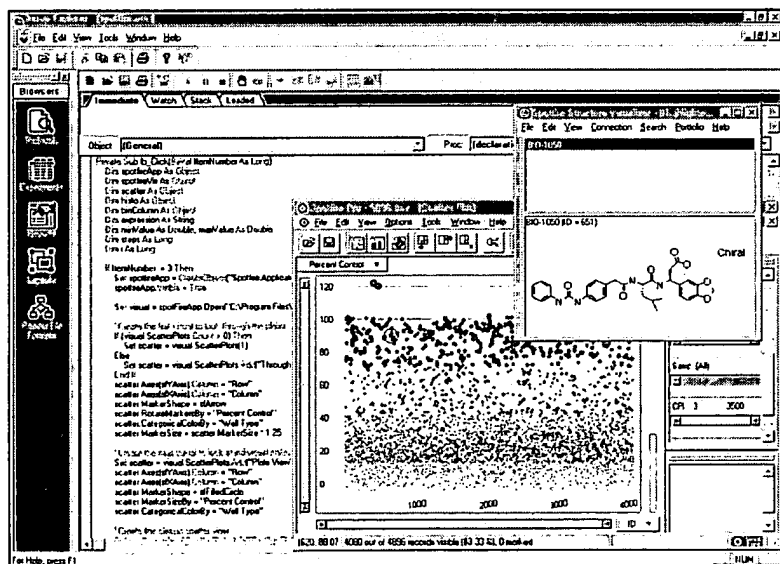
MDL has achieved this flexibility with result maps, abstraction layers that "map" variables and groups of variables to physical tables. Because the data model separates results display from data storage, system administrators have a great deal of flexibility in setting up tables, ranging from short and wide to tall and skinny displays. Scientists can create new variables themselves, and the results will be stored and easily retrievable. Meanwhile, administrators can fine-tune data storage to optimize performance, without disturbing the users.

In addition, Assay Explorer's exposed API, accessible through an integrated Visual Basic engine, helps organizations customize the software to work with their unique systems and workflows. Organizations can create add-ins to communicate with laboratory instrumentation, email status and results, create custom data entry screens, or perform any of a number of tasks. "The integrated VB engine and exposed API ensure that today's life science labs can embrace the newest automation and assay technologies quickly," Burns explained.

"Scientists will not feel Assay Explorer's components any more than they notice the underlying components that drive Microsoft Office applications," he continued. "What they will notice is that Assay Explorer fits their unique processes easily and effectively. If they ask their IT groups for a customization, it will happen quickly—much quicker than with other types of applications that they may have used up until now."

## Easier Experimental Setup and Analysis

For scientists at the bench, Assay Explorer can assist with managing protocols, experiments, and results. Instead of rigid results templates, Assay Explorer provides intuitive interfaces from which scientists can create any number of plate layouts,



Using Assay Explorer's integrated Visual Basic engine, IT staff can easily customize the system. The add-in shown here integrates Assay Explorer with Spotfire, Inc.'s Spotfire Pro, enabling scientists to transfer data seamlessly between the two programs. Other add-ins might connect Assay Explorer to image analysis packages, perform customized calculations, or provide automatic email notification.

continued on page 13

### Assay Explorer continued from page 11

reader formats, or calculations. Biologists then simply select the experimental protocol, layout, data files, and reader format and push, "Go." Assay Explorer does the rest, extracting data from the files, applying the layout, and calculating the experimental results.

In addition, Assay Explorer provides researchers with extensive protocol management capabilities, enabling them to create, store, retrieve, edit, version, and compare protocols. Scientists can evaluate their experiments by comparing experimental methods and results together. As a result, experimental analysis is more reliable, less error-prone, and faster, and scientists spend less time struggling with awkward templates or writing code, leaving more time for science.

Assay Explorer also gives scientists more control over how results are displayed, expediting communication throughout the enterprise. The system provides access to flexible graphics, querying tools, and display functions. Scientists can use these tools to create sophisticated reports and analyses, linking graphics, chemical structures, and other attachments directly to pertinent data.

### Easier Customization for More Powerful Applications

IT staffs, already overworked by the tremendous demands that modern discovery places on informatics, will find Assay Explorer a refreshing change from the norm. Customizing Assay Explorer and integrating it with existing data systems are handled through the integrated Visual Basic engine. Add-ins, for instance, can be easily built to handle specific tasks, such as performing a particular type of analysis or calculation, launching an external software package, or creating a custom report or query.

Assay Explorer also improves an organization's data consistency and searchability through its dictionary management capabilities. Dictionaries can enforce a common vocabulary throughout an enterprise, offering a standard nomenclature for assays, results, materials, and other information. Such a vocabulary ensures that scientists find all and only the information they need when they need it.

For a look at how Assay Explorer's built-in flexibility can be put to use in your laboratory, visit the Assay Explorer Web site at <http://www.mdli.com/ae> or call MDL at (888) 777-1002. ♦

### MDL Perspective continued from page 5

tools that will interact with our chemistry data cartridge. These projects should result in tools that will be released in the same timeframe as the chemistry data cartridge. We plan to continue this momentum in 2000, when we will introduce a series of applications that will exploit the chemistry data cartridge and other aspects of our new architecture. Three applications are planned: Compound Warehouse; the new Web client to Beilstein; and Library Workbook. Working with the new technology on applications under our control will give us time to ensure that we have optimized aspects such as performance, interaction, bandwidth, and scalability.

Supporting this work and other technology development at MDL is our new partnership with Sun. The most immediate result of this new relationship will be the introduction of Sun as a platform for our existing technology. We are porting all ISIS foundation technology to Sun, starting with ISIS/Host this year and continuing with Cheshire, Chemscape, and Central Library early in 2000. But customers will experience the most important ramifications of this relationship in 2000 with the release of our chemistry data cartridge and other pieces of the new architecture. At present, Sun has emerged as the principal development platform for Oracle. By working on the Sun platform now, we have the chance to view the data cartridge world the way Oracle sees it. The more we know about how Oracle is migrating their technology, the better prepared we will be to take advantage of the changes that affect our plans. ♦

### Toolboxes at UCB Research continued from page 9

For instance, the company is currently exploring Oracle for databasing both structures and relational data. The migration will involve a lot of work on the server side, but, because the desktop applications rely on components, the changes there will be minimal. In fact, with the increased data analysis demands that have resulted from the acquisition, UCB Research is considering whether or not to add other toolboxes to its system. "Our biologists are discovering the need for common data analysis tools, and the value of archiving and sharing their protocols," Toy-Palmer said. "We feel that the Data Analysis Toolbox and the Protocol Toolbox will play important roles in helping our users do their jobs better." ♦

## PRODUCT BRIEFS

- MDL released in September the first enhanced version of SCULPT since it acquired Interactive Simulations, Inc., last April. SCULPT 3.0 provides many new features requested by customers, including automatic 3D alignment of compounds, more visualization options, OLE embedding of 3D images, and tighter integration with other MDL products.
- Beilstein Information Systems announced in September the release of CrossFire EcoPharm, an add-on to the CrossFire System that brings together pharmacological, toxicological, and ecotoxicological data from 180 leading journals.
- MDL has included several customer-requested enhancements in the new releases of SMART (released in August) and Chemscape Server 1.5 (released in September).
- MDL released in August LitLink/Standard Server 1.1, an enhanced version of its electronic article broker that gives researchers one-click access to scientific literature and patent citations via MDL's Reaction Browser and Reaction Web database interfaces and Beilstein's Commander interface to CrossFire.
- The 99.1 release of Metabolite, which shipped in July, includes nonproprietary new drug application (NDA) information obtained through a 1997 material transfer agreement with the U.S. Food and Drug Administration. Other recent database updates are MDDR 99.1 (May), ACD 99.1 (June), ACD-SC 99.2 (July), CPI 99.1 (July), SPORE 99.3 (July), CIRX 99.2 (August), and CSM 99.2 (August).



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Set	Items	Description
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S2	1281473	TEMPLATE? ? OR LAYOUT? ? OR VIEW? ?
S3	963	S2(5N) (PREDETERMIN? OR PRESET? OR PREESTABLISH? OR PREDEFI- N? OR PREDESIGNATED OR PREARRANGED OR PRESCRIBED OR (PREVIOUS- LY OR PRE) () (DETERMIN? OR SET???? OR ESTABLISH? OR DEFIN? OR - DESIGNATED OR SCRIBED OR ARRANGED))
S4	736	(DEFAULT OR FIXED) (3W)S2
S5	6	S1 AND S3:S4
S6	4	RD (unique items)
S7	1636	S1 AND S2
S8	930	S1 AND TEMPLATE? ?
S9	25830	BIOLOGICAL(1W) (DATA OR INFORMATION)
S10	9	S9(10N)TEMPLATE? ?
S11	9	RD (unique items)

11/5/8 (Item 1 from file: 2)

DIALOG(R)File 2:INSPEC

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7604615 INSPEC Abstract Number: C2003-06-7330-138

**Title: Database strategies for genetic information and biological data**

Author(s): Dewey, F.

Author Affiliation: Dept. of Mech. Eng., MIT, Boston, MA, USA

Conference Title: Proceedings of the IEEE-EMBS Special Topic Conference on Molecular, Cellular and Tissue Engineering (Cat. No.02EX596) p.198

Publisher: IEEE, Piscataway, NJ, USA

Publication Date: 2002 Country of Publication: USA 211 pp.

ISBN: 0 7803 7557 2 Material Identity Number: XX-2002-04040

U.S. Copyright Clearance Center Code: 0-7803-7557-2/02/\$17.00

Conference Title: Proceedings of the IEEE-EMBS Special Topic Conference on Molecular, Cellular and Tissue Engineering

Conference Date: 6-9 June 2002 Conference Location: Genoa, Italy

Language: English Document Type: Conference Paper (PA)

Treatment: Applications (A); Practical (P)

Abstract: Summary form only given. Two key characteristics of modern biological research are: (a) the experimental data collections are very large and difficult to interpret; and (b) data interpretation generally requires information from genetic and other databases that are distinct from the ones in which the experimental data are stored. I discuss current strategies for constructing a database federation that can support composite queries that require data from different databases. I discuss current efforts to construct reusable software **templates** for **biological data** that makes querying and extracting data from different experimental databases much easier. The role of XML and various transport and interface mechanisms (TCP/IP, CORBA, Java) are also covered.

Subfile: C

Descriptors: biology computing; distributed databases; hypermedia markup languages; medical information systems; query processing; software reusability; very large databases

Identifiers: genetic information; composite queries; reusable software templates; querying; experimental databases; XML; TCP/IP; CORBA; biological data; very large database; experimental data collections; data interpretation; database federation

Class Codes: C7330 (Biology and medical computing); C6160B (Distributed databases); C7140 (Medical administration); C6160Z (Other DBMS)

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Set	Items	Description
S1	23991	BIOLOGICAL(1W) (DATA OR INFORMATION) (1W)MANAG? OR BIOINFORM- ATIC? ?
S2	2917189	TEMPLATE? ? OR LAYOUT? ? OR VIEW? ?
S3	6216	S2(5N) (PREDETERMIN? OR PRESET? OR PREESTABLISH? OR PREDEFI- N? OR PREDESIGNATED OR PREARRANGED OR PRESCRIBED OR (PREVIOUS- LY OR PRE) () (DETERMIN? OR SET???? OR ESTABLISH? OR DEFIN? OR - DESIGNATED OR SCRIBED OR ARRANGED))
S4	2873	(DEFAULT OR FIXED) (3W)S2
S5	0	S1(50N)S3:S4
S6	4	S1(100N)S3:S4
S7	536	S1(50N)S2
S8	1	RD S6 (unique items)
S9	1428	SPOTFIRE
S10	31	S1(100N)S2(100N)S9
S11	11	RD (unique items)
S12	53	S1(50N)TEMPLATE? ?
S13	24	RD (unique items)

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**Ames Color-File Releases New HIPAA Products for Healthcare Industry; New  
Ames Color-File Products Help Healthcare Records Industry Meet  
Approaching HIPAA Compliance Deadline.**  
Business Wire, p2225  
Dec 18, 2002  
Language: English Record Type: Fulltext  
Document Type: Newswire; Trade  
Word Count: 366

... the contents of the files.

-- HIPAA Compliance Resource Center (HCRC): A comprehensive software solution developed by Clinical **BioInformatics** Consulting, Inc., that provides important HIPAA guidelines in a user-friendly format; computer-based training (with administrative tracking features); **templates** for GAP analysis, compliance implementation plans, and other required documents; and links to numerous HIPAA Web resources...

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03217517 Supplier Number: 88599197 (USE FORMAT 7 FOR FULLTEXT)  
**Biotique Systems Announces Three Initial Customers for its BLIS Genomic  
Integration Solution.**  
Business Wire, p0080  
July 9, 2002  
Language: English Record Type: Fulltext  
Document Type: Newswire; Trade  
Word Count: 544

... pharmaceutical and biotechnology companies to expedite target discovery and refinement using the human genome as a reference **template**.  
"BLIS allows any biologist working in drug discovery at Bristol-Myers Squibb Company to visualize our proprietary annotations to human genomic data," said Dr. Dan Davison, associate director of **bioinformatics**, applied genomics, Bristol-Myers Squibb Company. "We wanted to implement public genomic data and genome browsers in..."

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03016079 Supplier Number: 79162411 (USE FORMAT 7 FOR FULLTEXT)  
**Structural GenomiX Appoints Stephen K. Burley as Chief Scientific Officer.**  
PR Newswire, pNA  
Oct 16, 2001  
Language: English Record Type: Fulltext  
Document Type: Newswire; Trade  
Word Count: 714

... Board members.

SGX is a leader in experimental and computational structural biology, transforming genomic information into structural **templates** for drug discovery. SGX technologies include advanced **bioinformatics** tools for target selection and structure-based functional annotation, automation of molecular biology and protein biochemistry, high...

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03011029 Supplier Number: 79041445 (USE FORMAT 7 FOR FULLTEXT)  
**Structural GenomiX Names Mike Grey Chief Business Officer.**  
PR Newswire, pNA  
Oct 9, 2001  
Language: English Record Type: Fulltext  
Document Type: Newswire; Trade  
Word Count: 550

... exceptional company."  
SGX is a leader in experimental and computational structural biology, transforming genomic information into structural **templates** for drug discovery. SGX technologies include advanced **bioinformatics** tools for target selection and structure-based functional annotation, automation of molecular biology and protein biochemistry, high...

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**Structural GenomiX Adds Two Board Members.**  
PR Newswire, pNA  
July 19, 2001  
Language: English Record Type: Fulltext  
Document Type: Newswire; Trade  
Word Count: 507

... Structural GenomiX (SGX) is a leader in experimental and computational structural biology, transforming genomic information into structural **templates** for drug discovery. The company's industrialized gene-to-structure pipeline incorporates innovative technologies to streamline protein structure determination. These technologies include advanced **bioinformatics** tools for target selection and structure annotation, automation of molecular biology and protein biochemistry, high-throughput crystallization...

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02707540 Supplier Number: 66574005 (USE FORMAT 7 FOR FULLTEXT)  
**Genomica's Discovery Manager (TM) Software Licensed to Aventis Pharma.**  
PR Newswire, p9216  
Nov 2, 2000  
Language: English Record Type: Fulltext  
Document Type: Newswire; Trade  
Word Count: 993

... strength of Discovery Manager's sequence analysis technology."  
About Discovery Manager  
Discovery Manager is Genomica's core **bioinformatics** product that enables individual or collaborating researchers to access, store, manipulate, analyze, annotate and integrate genomic data from a variety of sources. The product is an integrated suite of software tools and a database **template** for genomics research. The database can be filled with genomic data from the user's own research...

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DIALOG(R)File 621:Gale Group New Prod.Annou.(R)  
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02660443      Supplier Number: 65505909    (USE FORMAT 7 FOR FULLTEXT)  
**Genome Therapeutics Licenses Genomica's Discovery Manager(TM) Software.**  
PR Newswire, pNA  
Sept 27, 2000  
Language: English      Record Type: Fulltext  
Document Type: Newswire; Trade  
Word Count:      659

...      and our own custom analysis and display programs."

    About Discovery Manager

    Discovery Manager is Genomica's core **bioinformatics** product. It has been designed over the past 15 years by Thomas G. Marr, Ph.D., our...

...in the field of genomics. The product is an integrated suite of software tools and a database **template** for genomics research. The database can be filled with genomic data from the user's own research...

13/3,K/8      (Item 8 from file: 621)  
DIALOG(R)File 621:Gale Group New Prod.Annou. (R)  
(c) 2005 The Gale Group. All rts. reserv.

02590196      Supplier Number: 63741735    (USE FORMAT 7 FOR FULLTEXT)  
**Genomica Wins Prestigious Innovation Award for Discovery Manager(TM) Software.**  
PR Newswire, p0601  
July 28, 2000  
Language: English      Record Type: Fulltext  
Document Type: Newswire; Trade  
Word Count:      515

...      be read online at <http://www.bcbr.com>.

    About Discovery Manager

    Discovery Manager is Genomica's core **bioinformatics** product. It has been developed over the past 15 years by our chief scientist in collaboration with...

...in the field of genomics. The product is an integrated suite of software tools and a database **template** for genomics research. The database can be filled with genomic data from the user's own research...

13/3,K/9      (Item 9 from file: 621)  
DIALOG(R)File 621:Gale Group New Prod.Annou. (R)  
(c) 2005 The Gale Group. All rts. reserv.

02553368      Supplier Number: 62987653    (USE FORMAT 7 FOR FULLTEXT)  
**Genomica's Enhanced Discovery Manager(TM) Software Launched to Provide Critical Tools for Genomics Research.**  
PR Newswire, pNA  
June 27, 2000  
Language: English      Record Type: Fulltext  
Document Type: Newswire; Trade  
Word Count:      580

...      for easier manipulation and analysis of twin data.

    About Discovery Manager

    Discovery Manager is Genomica's core **bioinformatics** product. It has been developed over the past 15 years by our chief scientist in collaboration with...

...in the field of genomics. The product is an integrated suite of software tools and a database **template** for genomics research. The database can be filled with genomic data from the user's own research...

13/3,K/10      (Item 10 from file: 621)  
DIALOG(R)File 621:Gale Group New Prod.Annou. (R)

(c) 2005 The Gale Group. All rts. reserv.

02542400 Supplier Number: 62794475 (USE FORMAT 7 FOR FULLTEXT)  
**Genomica Licenses Discovery Manager(TM) Software to the National Institutes of Health's Craniofacial Epidemiology and Genetics Branch.**  
PR Newswire, pNA  
June 19, 2000  
Language: English Record Type: Fulltext  
Document Type: Newswire; Trade  
Word Count: 579

... cancer, cleft lip and palate and periodontal disease.

About Discovery Manager

Discovery Manager is Genomica's core **bioinformatics** product. It has been developed over the past 15 years by our chief scientist in collaboration with...

...in the field of genomics. The product is an integrated suite of software tools and a database **template** for genomics research. The database can be filled with genomic data from the user's own research...

13/3,K/11 (Item 11 from file: 621)  
DIALOG(R)File 621:Gale Group New Prod.Annou.(R)  
(c) 2005 The Gale Group. All rts. reserv.

01682956 Supplier Number: 50201555 (USE FORMAT 7 FOR FULLTEXT)  
**SBI's Protein Structure Directed Combinatorial Chemistry Cuts Time and Cost 100x for Synthesis of New Anti-Inflammatory Drug Lead Molecules**  
PR Newswire, p727LAM012  
July 27, 1998  
Language: English Record Type: Fulltext  
Article Type: Article  
Document Type: Newswire; Trade  
Word Count: 483

SAN DIEGO, Calif., July 27 /PRNewswire/ -- Structural **Bioinformatics** Inc. ("SBI"), San Diego has successfully combined its computational technologies covering dynamic protein surface generation and analysis, dynamic pharmacophore **template** generation (SBI's DynaPharm(TM) technology) and protein structure-guided virtual combinatorial library generation (SBI's CombiLib...

13/3,K/12 (Item 1 from file: 636)  
DIALOG(R)File 636:Gale Group Newsletter DB(TM)  
(c) 2005 The Gale Group. All rts. reserv.

05413856 Supplier Number: 94202039 (USE FORMAT 7 FOR FULLTEXT)  
**Pharmacogenomics: Finding the competitive edge in genetic variation.**  
M2 Presswire, pNA  
Nov 13, 2002  
Language: English Record Type: Fulltext  
Document Type: Newswire; Trade  
Word Count: 2253

... of Pharmacogenomic Datarmacology at PharmaciaDr. Russ Altman of the Stanford Medical InformaticsGroup 8.1 Origins of a **Bioinformatics** Tool for Pharmacogenetics 8.2 Architecture of the RiboWeb System 8.3 The Importance of Ontologies and Standardized Vocabularies 8.4 Structured Experimental **Templates** 8.5 What Is Pharmacogenetics? 8.6 Management of Pharmacogenetics-Related Data Overview of the NIH's...

13/3,K/13 (Item 2 from file: 636)  
DIALOG(R)File 636:Gale Group Newsletter DB(TM)  
(c) 2005 The Gale Group. All rts. reserv.

04952733      Supplier Number: 72732893    (USE FORMAT 7 FOR FULLTEXT)  
**Amersham Pharmacia Biotech.**  
Instrument Business Outlook, v9, n22, p8  
Feb 28, 2001  
Language: English      Record Type: Fulltext  
Document Type: Newsletter; Trade  
Word Count:    298

...      base of over 700 units worldwide.

Upcoming product releases for drug discovery include the TempliPhi for sequencing **template** preparation and SnuPe for SNP analysis. For drug screening and **bioinformatics**, the company will also introduce FARcyte for lower-throughput screening and its Laboratory Workflow Systems software later...

13/3,K/14      (Item 3 from file: 636)  
DIALOG(R)File 636:Gale Group Newsletter DB(TM)  
(c) 2005 The Gale Group. All rts. reserv.

03669448      Supplier Number: 47905383    (USE FORMAT 7 FOR FULLTEXT)  
**STRUCTURAL BIOINFORMATICS SIGNS ALLIANCE WITH BIOCHEM PHARMA**  
BIOWORLD Today, v8, n155, pN/A  
August 12, 1997  
Language: English      Record Type: Fulltext  
Document Type: Magazine/Journal; Trade  
Word Count:    240

...      pathway, which if blocked would trigger apoptosis, or cell death.

In both hepatitis C and cancer, Structural **Bioinformatics** already knows the 3-D construction of the targeted proteins. The company will use its technology to refine details of the structure and pinpoint the active sites, which determine the design of **template** compounds that interact with or mimic the proteins. Those **templates** then are used to search computer-based virtual chemical libraries or real libraries for drug candidates.

By...

13/3,K/15      (Item 4 from file: 636)  
DIALOG(R)File 636:Gale Group Newsletter DB(TM)  
(c) 2005 The Gale Group. All rts. reserv.

03265402      Supplier Number: 46701156    (USE FORMAT 7 FOR FULLTEXT)  
**STRUCTURAL BIOINFORMATICS BUILDS 3-D PROTEINS FROM GENE SEQUENCES**  
BIOWORLD Today, v7, n177, pN/A  
Sept 11, 1996  
Language: English      Record Type: Fulltext  
Document Type: Magazine/Journal; Trade  
Word Count:    592

...      what lobes of the protein move, he observed, improves the accuracy of drug design.

In addition, Structural **Bioinformatics** ' software identifies points on the protein that provide the most likely site of interaction for a therapeutic compound, assisting drug designers in making a **template** molecule to create a combinatorial library.

"We give them the protein structure and tell them where to look on it to make their drug," Maggio said.

Structural **Bioinformatics**, however, has not yet solved the dynamics of protein folding, Maggio added, and for that reason the...

13/3,K/16      (Item 1 from file: 148)  
DIALOG(R)File 148:Gale Group Trade & Industry DB  
(c)2005 The Gale Group. All rts. reserv.



11489232 SUPPLIER NUMBER: 56752941 (USE FORMAT 7 OR 9 FOR FULL TEXT)

**Mutations in the ABC1 gene in familial HDL deficiency with defective cholesterol efflux. (Statistical Data Included)**

Marcil, Michel; Brooks-Wilson, Angela; Clee, Susanne M; Roomp, Kirsten; Zhang, Lin-Hua; Yu, Lu; Collins, Jennifer A; van Dam, Marjel; Molhuizen, Henri O F; Loubster, Odell; Ouellette, B F Francis; Sensen, Christoph W; Fichter, Keith; Mott, Stephanie; Denis, Maxime; Boucher, Betsie; Pimstone, Simon; Genest Jr, Jacques; Kastelein, John J P; Hayden, Michael R  
Lancet, 354, 9187, 1341

Oct 16, 1999

DOCUMENT TYPE: Statistical Data Included ISSN: 0099-5355

LANGUAGE: English RECORD TYPE: Fulltext; Abstract

WORD COUNT: 4677 LINE COUNT: 00387

... 25: 3389-402.

(23) Schuler GD. Sequence alignment and database searching. In: Baxevanis AD, Ouellette BFF, ed. **Bioinformatics** : a practical guide to the analysis of genes and proteins. New York: Wiley and Sons, 1998: 145-71.

(24) Rosenthal A, Coutelle O, Craxton M. Large-scale production of DNA sequencing **templates** by microtitre format PCR. Nucleic Acids Res 1993; 21: 173-74

(25) Genest Jr J, Martin-Munley...

13/3,K/17 (Item 2 from file: 148)

DIALOG(R)File 148:Gale Group Trade & Industry DB

(c)2005 The Gale Group. All rts. reserv.

07313245 SUPPLIER NUMBER: 15511764 (USE FORMAT 7 OR 9 FOR FULL TEXT)

**GENSET AND GENETHON TO LAUNCH MAJOR JOINT PROGRAM TO SEQUENCE AND ANALYZE HUMAN GENOME REGULATORY CODE**

PR Newswire, p0629NY008

June 29, 1994

LANGUAGE: ENGLISH RECORD TYPE: FULLTEXT

WORD COUNT: 931 LINE COUNT: 00078

... said Bernard Barataud, President of Genethon. "These organizations' complementary technologies in the fields of mapping, sequencing, automation, **bioinformatics**, and industrial-scale project management give the TGS program a distinct advantage in analyzing the regulatory code...

...and Genethon will provide the program with several proprietary techniques for use in identifying and labeling specific **templates** for regulatory regions."

Under the terms of the agreement, the two organizations have made an initial commitment...

13/3,K/18 (Item 1 from file: 624)

DIALOG(R)File 624:McGraw-Hill Publications

(c) 2005 McGraw-Hill Co. Inc. All rts. reserv.

01298484

**Seeking better vectors**

By SL

Biotechnology Newswatch, Vol. 91, No. 6, Pg 2

December 2, 2002

JOURNAL CODE: BIO

SECTION HEADING: BUSINESS BRIEFS ISSN: 0275-3687

WORD COUNT: 308

TEXT:

... of ones with high stability and that contribute to high levels of expression.

Using sequence data and **bioinformatics**, company scientists have identified a very powerful, 36 base pair origin and tested it in a range...

...audience.

They hope to test this and other versions of a 36-base pair ``consensus sequence, '' or **template**, with therapeutic or corrective genes in a range of vectors from disarmed viruses to naked DNA or...

13/3,K/19 (Item 1 from file: 610)  
DIALOG(R)File 610:Business Wire  
(c) 2005 Business Wire. All rts. reserv.

00195535 20000215046B0410 (USE FORMAT 7 FOR FULLTEXT)  
**Lark Announces Revenue Growth for 1999 and Move to Expanded Facilities**  
Business Wire  
Tuesday, February 15, 2000 13:46 EST  
JOURNAL CODE: BW LANGUAGE: ENGLISH RECORD TYPE: FULLTEXT  
DOCUMENT TYPE: NEWSWIRE  
WORD COUNT: 529

TEXT:  
...Board of Directors recently approved the purchase of new equipment to increase our capacity to produce DNA **templates** and sequencing. Second, on February 1st, we hired Dr. Wei Wang as Director of **Bioinformatics** to manage our increased flow of genomic data, preparing Lark for innovative changes in the way we...

13/3,K/20 (Item 1 from file: 613)  
DIALOG(R)File 613:PR Newswire  
(c) 2005 PR Newswire Association Inc. All rts. reserv.

00657998 20011016NYTU036 (USE FORMAT 7 FOR FULLTEXT)  
**Structural Genomix Appoints Chief Scientific OfficerLeaderCall**  
PR Newswire  
Tuesday, October 16, 2001 08:02 EDT  
JOURNAL CODE: PR LANGUAGE: ENGLISH RECORD TYPE: FULLTEXT  
DOCUMENT TYPE: NEWSWIRE  
WORD COUNT: 711

TEXT:  
...Board members.  
SGX is a leader in experimental and computational structural biology, transforming genomic information into structural **templates** for drug discovery. SGX technologies include advanced **bioinformatics** tools for target selection and structure-based functional annotation, automation of molecular biology and protein biochemistry, high...

13/3,K/21 (Item 2 from file: 613)  
DIALOG(R)File 613:PR Newswire  
(c) 2005 PR Newswire Association Inc. All rts. reserv.

00654020 20011009NYTU035 (USE FORMAT 7 FOR FULLTEXT)  
**Structural Genomix Names Mike Grey Chief Business Officernf And 'Try On'**  
PR Newswire  
Tuesday, October 9, 2001 08:07 EDT  
JOURNAL CODE: PR LANGUAGE: ENGLISH RECORD TYPE: FULLTEXT  
DOCUMENT TYPE: NEWSWIRE  
WORD COUNT: 560

TEXT:

...exceptional company."

SGX is a leader in experimental and computational structural biology, transforming genomic information into structural **templates** for drug discovery. SGX technologies include advanced **bioinformatics** tools for target selection and structure-based functional annotation, automation of molecular biology and protein biochemistry, high...

13/3,K/22 (Item 3 from file: 613)

DIALOG(R)File 613:PR Newswire

(c) 2005 PR Newswire Association Inc. All rts. reserv.

00649281 20011001HSM030 (USE FORMAT 7 FOR FULLTEXT)

**Structural GenomiX and Celera Sign Agreement**

PR Newswire

Monday, October 1, 2001 07:32 EDT

JOURNAL CODE: PR LANGUAGE: ENGLISH RECORD TYPE: FULLTEXT

DOCUMENT TYPE: NEWSWIRE

WORD COUNT: 806

Structural GenomiX (SGX) is a leader in experimental and computational structural biology, transforming genomic information into structural **templates** for drug discovery. SGX technologies include advanced **bioinformatics** tools for target selection and structure-based functional annotation, automation of molecular biology and protein biochemistry, high...

13/3,K/23 (Item 4 from file: 613)

DIALOG(R)File 613:PR Newswire

(c) 2005 PR Newswire Association Inc. All rts. reserv.

00646494 20010925NYTU049 (USE FORMAT 7 FOR FULLTEXT)

**Structural GenomiX-Funded Undulator Beamline Op. Nov. 2001**

PR Newswire

Tuesday, September 25, 2001 07:31 EDT

JOURNAL CODE: PR LANGUAGE: ENGLISH RECORD TYPE: FULLTEXT

DOCUMENT TYPE: NEWSWIRE

WORD COUNT: 726

TEXT:

...Structural GenomiX (SGX) is a leader in experimental and computational structural biology, transforming genomic information into structural **templates** for drug discovery. SGX technologies include advanced **bioinformatics** tools for target selection and structure-based functional annotation, automation of molecular biology and protein biochemistry, high...

13/3,K/24 (Item 5 from file: 613)

DIALOG(R)File 613:PR Newswire

(c) 2005 PR Newswire Association Inc. All rts. reserv.

00644540 20010920NYTH031 (USE FORMAT 7 FOR FULLTEXT)

**Structural Genomix and Compaq to Build Multi-Million Dollartatives**

PR Newswire

Thursday, September 20, 2001 07:31 EDT

JOURNAL CODE: PR LANGUAGE: ENGLISH RECORD TYPE: FULLTEXT

DOCUMENT TYPE: NEWSWIRE

WORD COUNT: 682

TEXT:

...Structural GenomiX (SGX) is a leader in experimental and computational structural biology, transforming genomic information into structural **templates** for drug discovery. SGX technologies include advanced **bioinformatics** tools for target selection and structure annotation, automation of molecular biology and protein biochemistry, high-throughput crystallization...

File 347:JAPIO Nov 1976-2004/Oct(Updated 050209)

(c) 2005 JPO & JAPIO

File 350:Derwent WPIX 1963-2005/UD,UM &UP=200514

(c) 2005 Thomson Derwent

Set	Items	Description
S1	298	BIOLOGICAL(1W)(DATA OR INFORMATION)(1W)MANAG? OR BIOINFORM- ATIC? ?
S2	1579460	TEMPLATE? ? OR LAYOUT? ? OR VIEW? ?
S3	2754	S2(5N)(PREDETERMIN? OR PRESET? OR PREESTABLISH? OR PREDEFI- N? OR PREDESIGNATED OR PREARRANGED OR PRESCRIBED OR (PREVIOUS- LY OR PRE)() (DETERMIN? OR SET???? OR ESTABLISH? OR DEFIN? OR - DESIGNATED OR SCRIBED OR ARRANGED))
S4	812	(DEFAULT OR FIXED)(3W)S2
S5	1	S1 AND S3:S4
S6	36	S1 AND S2
S7	26	BIO()INFORMATIC? ?
S8	5	S2 AND S7
S9	4	S8 NOT S6
S10	113	PA='KENT RIDGE DIGITAL LABS'
S11	2	(S1 OR S7) AND S10

6/5/5 (Item 5 from file: 350)  
DIALOG(R)File 350:Derwent WPIX  
(c) 2005 Thomson Derwent. All rts. reserv.

016137891 \*\*Image available\*\*  
WPI Acc No: 2004-295767/200427  
XRPX Acc No: N04-234916

Computer-based data analysis system for medical diagnostic applications,  
has analytical engine that is executable on computer and is linked to  
data management system for accessing and processing knowledge elements

Patent Assignee: ISMARTSOFT INC (ISMA-N); SAYAD S (SAYA-I)

Inventor: SAYAD S

Number of Countries: 105 Number of Patents: 003

Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
WO 200429828	A2	20040408	WO 2003CA1450	A	20030923	200427 B
US 20040153430	A1	20040805	US 2002412810	P	20020924	200452
			US 2003668354	A	20030924	
AU 2003271441	A1	20040419	AU 2003271441	A	20030923	200462

Priority Applications (No Type Date): US 2002412810 P 20020924; US  
2003668354 A 20030924

Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
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WO 200429828	A2	E	82	G06F-017/30	
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Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA  
CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN  
IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NI NO  
NZ OM PG PH PL PT RO RU SC SD SE SG SK SL SY TJ TM TN TR TT TZ UA UG US  
UZ VC VN YU ZA ZM ZW

Designated States (Regional): AT BE BG CH CY CZ DE DK EA EE ES FI FR GB  
GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ  
UG ZM ZW

US 20040153430	A1			H04B-001/74	Provisional application US 2002412810
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AU 2003271441	A1			G06F-017/30	Based on patent WO 200429828
---------------	----	--	--	-------------	------------------------------

Abstract (Basic): WO 200429828 A2

NOVELTY - An analytical engine executed by a computer, provides  
multiple knowledge elements including records and/or variables from  
other more data sources. The analytical engine is linked to data  
management system, for accessing and processing the knowledge elements.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the  
following:

- (1) data analysis method;
- (2) method of enabling parallel processing;
- (3) method of enabling scenario testing;
- (4) method of enabling dimension reduction;
- (5) method of enabling dynamic queries;
- (6) method of enabling distributed processing; and
- (7) computer program product for enabling data analysis and process

control.

USE - For data mining, statistical analysis, artificial  
intelligence, machine learning and process control for providing  
information for real-world applications like medical diagnostic  
applications for monitoring abnormality of deceases and heat failure,  
mobile applications for process monitoring and control in industrial  
applications e.g. for dryer, banking and credit scoring applications,  
**bioinformatic** and pharmaceutical solutions, e-commerce and CRM  
applications, fraud detection applications, health care and human  
resources, privacy and security applications, sports and entertainment  
application, stock and investment analysis and business sales  
prediction, telecom, instrumentation and machinery and traveling  
applications, prediction of start codon in genomes like DNA and RNA,  
principal component analysis, and for control of robotic arm.

ADVANTAGE - Knowledge entity is efficiently updated with new  
records by matrix addition. Variables can be added or removed from  
knowledge entity by adding or removing set of cells, such as row or

column to one or both dimensions. Enables to immediately utilize new data, purposefully ignore some data, incorporate new variables in knowledge entity.

DESCRIPTION OF DRAWING(S) - The figure shows a schematic view of processing apparatus.

dryer (10)  
feed tube (12)  
heater (16)  
chamber (30)  
plenum (32)  
pp; 82 DwgNo 1/12

Title Terms: COMPUTER; BASED; DATA; ANALYSE; SYSTEM; MEDICAL; DIAGNOSE;  
APPLY; ANALYSE; ENGINE; EXECUTE; COMPUTER; LINK; DATA; MANAGEMENT; SYSTEM  
; ACCESS; PROCESS; ELEMENT

Derwent Class: T01

International Patent Class (Main): G06F-017/30; H04B-001/74

File Segment: EPI

6/5/12 (Item 12 from file: 350)

DIALOG(R)File 350:Derwent WPIX

(c) 2005 Thomson Derwent. All rts. reserv.

014668748 \*\*Image available\*\*

WPI Acc No: 2002-489452/200252

Related WPI Acc No: 2003-247127; 2004-041065; 2004-803926

XRFX Acc No: N02-386954

Biological experiment information management method for computer system, involves determining value for identifier input by user and included in generated template which is related to use of probe array

Patent Assignee: BERNHART D (BERN-I); NIJOR R S (NIJO-I)

Inventor: BERNHART D; NIJOR R S

Number of Countries: 001 Number of Patents: 001

Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
US 20020059326	A1	20020516	US 2000220587	P	20000725	200252 B
			US 2000220645	P	20000725	
			US 2000226999	P	20000822	
			US 2001273231	P	20010302	
			US 2001682098	A	20010719	

Priority Applications (No Type Date): US 2001682098 A 20010719; US  
2000220587 P 20000725; US 2000220645 P 20000725; US 2000226999 P 20000822  
; US 2001273231 P 20010302

Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
US 20020059326	A1		18	G06F-012/00	Provisional application US 2000220587

Provisional application US 2000220645  
Provisional application US 2000226999  
Provisional application US 2001273231

Abstract (Basic): US 20020059326 A1

NOVELTY - Several attributes are specified for each of the experiment identifiers input by a user. A data **template** is generated including the identifiers. A value for the identifier is determined with the specified attributes, using the generated **template** which is related to the use of probe array.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following:

- (1) Computer program product for **biological experiment information management** ; and
- (2) Computer implemented system for managing information of probe array experiment.

USE - For managing experimental data using computer system.

ADVANTAGE - Organizes, accesses and analyzes the various amount of information collected using nucleic acid probe arrays or using other probe arrays. The user can efficiently manage the complicated

experimental information with ease.

DESCRIPTION OF DRAWING(S) - The figure shows the simplified graphical representation of data flow in probe array assay.

pp; 18 DwgNo 2/6

Title Terms: BIOLOGICAL; EXPERIMENT; INFORMATION; MANAGEMENT; METHOD; COMPUTER; SYSTEM; DETERMINE; VALUE; IDENTIFY; INPUT; USER; GENERATE;

TEMPLATE ; RELATED; PROBE; ARRAY

Derwent Class: S05; T01

International Patent Class (Main): G06F-012/00

File Segment: EPI

6/5/13 (Item 13 from file: 350)

DIALOG(R)File 350:Derwent WPIX

(c) 2005 Thomson Derwent. All rts. reserv.

014642806 \*\*Image available\*\*

WPI Acc No: 2002-463510/200249

XRAM Acc No: C02-131840

XRPX Acc No: N02-365399

Computerized software platform for integrating object based data models

uses CORBA and provides services to components from selected requests

Patent Assignee: NAT CENT GENOME RESOURCES (NAGE-N)

Number of Countries: 097 Number of Patents: 002

Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
WO 200239486	A2	20020516	WO 2001US49984	A	20011109	200249 B
AU 200232761	A	20020521	AU 200232761	A	20011109	200260

Priority Applications (No Type Date): US 2000709158 A 20001109

Patent Details:

Patent No Kind Lan Pg Main IPC Filing Notes

WO 200239486 A2 E 39 H01L-000/00

Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA  
CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN  
IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ  
OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW  
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR  
IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

AU 200232761 A H01L-000/00 Based on patent WO 200239486

Abstract (Basic): WO 200239486 A2

NOVELTY - Computerized software platform (I) uses common object request broker architecture (CORBA) comprising a client environment interfacing a user and a client bus maintaining connection between software components unaware of one another, is new.

USE - (I) is useful for integrating object based data models (claimed).

ADVANTAGE - The integrated system comprising object-based, computing software platform enables genomic researchers and bioinformaticians to access and utilize disparate **bioinformatic** software tools and data sources in a seamless, unified environment. The brokers provides services analogous to methods rather than servers with specific interfaces.

DESCRIPTION OF DRAWING(S) - The figure shows a schematic view of the typical steps a scientist might take for the simple **bioinformatic** research task.

pp; 39 DwgNo 1/11

Title Terms: COMPUTER; SOFTWARE; PLATFORM; INTEGRATE; OBJECT; BASED; DATA; MODEL; SERVICE; COMPONENT; SELECT; REQUEST

Derwent Class: B04; D16; T01

International Patent Class (Main): H01L-000/00

File Segment: CPI; EPI

6/5/14 (Item 14 from file: 350)

DIALOG(R)File 350:Derwent WPIX

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014551355     \*\*Image available\*\*  
WPI Acc No: 2002-372058/200240  
XRAM Acc No: C02-105322  
XRPX Acc No: N02-290748

**Computer system for creating bio-informatics database, e.g. immunological database has library of re-usable templates and user interface**

Patent Assignee: KENT RIDGE DIGITAL LABS (KENT-N)

Inventor: BRUSIC V; KOH L Y J; SCHONBACH C

Number of Countries: 003    Number of Patents: 002

Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
WO 200225564	A1	20020328	WO 2000SG155	A	20000925	200240    B
GB 2383452	A	20030625	WO 2000SG155	A	20000925	200341
			GB 20036836	A	20030325	

Priority Applications (No Type Date): WO 2000SG155 A 20000925

Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
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WO 200225564	A1	E	38	G06F-019/00	
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Designated States (National): GB SG US

GB 2383452	A	G06F-017/30	Based on patent WO 200225564
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Abstract (Basic): WO 200225564 A1

NOVELTY - A computer system includes a library of re-usable **templates** for establishing structure for a bio-informatics database. A user interface allows the extraction of information and analysis of data in the bio-informatics database. The bio-informatics database has records comprising sequence records using a dimensional model that identifies **view** (s) to data.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) creation of multiple related bio-informatics databases comprising selecting a main **template**, defining a main interface page outlay, establishing a library of re-usable **templates** to enable a structure for the **bioinformatics** database to be established, and then linking the **templates**; and

(2) a graphical user interface for use in creating multiple related bio-informatics databases. The user interface comprises a first polygonal area and polygonal areas contained within the first polygonal area. The contained polygonal areas include a second polygonal area for displaying fitter of selected **templates** and a third polygonal area for specifying the data to be entered on the database.

USE - The computer system is used to create bio-informatics database, e.g. immunological database or MHC-molecule-related database. The bio-informatics database is used for knowledge discovery and data mining applications.

ADVANTAGE - The inventive system efficiently creates bio-informatics databases that concentrate on a particular subject within the bio-informatics field (claimed).

DESCRIPTION OF DRAWING(S) - The figure shows the general arrangement of the computer system.

pp; 38 DwgNo 1/10

Title Terms: COMPUTER; SYSTEM; BIO; DATABASE; IMMUNOLOGICAL; DATABASE;

LIBRARY; **TEMPLATE**; USER; INTERFACE

Derwent Class: B04; D16; T01

International Patent Class (Main): G06F-017/30; G06F-019/00

File Segment: CPI; EPI

6/5/17        (Item 17 from file: 350)

DIALOG(R)File 350:Derwent WPIX

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014447058     \*\*Image available\*\*  
WPI Acc No: 2002-267761/200231  
Related WPI Acc No: 1999-060565  
XRAM Acc No: C02-079561

XRPX Acc No: N02-208228

**Research system for facilitating drug discovery and design comprises at least two computers for respectively running multi-platform object oriented programming code and storing vertical market specific data, and network architecture**

Patent Assignee: DICKSON M C (DICK-I); FORSCH D A (FORS-I); GLYNIAS M J (GLYN-I); O' DELL J (DELL-I); SOCLOF M S (SOCL-I); LION BIOSCIENCE AG (LION-N)

Inventor: DICKSON M C; FORSCH D A; GLYNIAS M J; O' DELL J; SOCLOF M S; O'DELL J M

Number of Countries: 001 Number of Patents: 002

Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
US 20020029255	A1	20020307	US 97873217	A	19970611	200231 B
			US 9895083	A	19980610	
US 6453333	B1	20020917	US 97873217	A	19970611	200264
			US 9895083	A	19980610	

Priority Applications (No Type Date): US 9895083 A 19980610; US 97873217 A 19970611

Patent Details:

Patent No	Kind	Lan Pg	Main IPC	Filing Notes
US 20020029255	A1	34	G06F-015/16	CIP of application US 97873217
US 6453333	B1		G06F-013/00	CIP of application US 97873217 CIP of patent US 6125383

Abstract (Basic): US 20020029255 A1

**NOVELTY** - Research system has at least two computers to respectively run a multi-platform object oriented programming code and store vertical market specific data. The computers are coupled by a network architecture allowing objects to transparently communicate with each other and affording the second computer access to the programming code and the vertical market specific data.

**DETAILED DESCRIPTION** - An **INDEPENDENT CLAIM** is also included for a method to perform informatics based research, which comprises using a first computer running a multi-platform object oriented programming code and operatively coupled to a network backbone, using a second computer having stored on it vertical market specific data and operatively coupled to the network backbone, using a network architecture to network the first and second computers to form a research system, and using the research system to integrate and organize the vertical market specific data to facilitate research.

**USE** - The research system, i.e. **bioinformatics** or chemi-informatics research system, is used for integrating and organizing biological and/or chemical data to facilitate drug discovery and design. It may be employed in a vertical market, e.g. the financial arena where large amounts of financial data are worked with.

**ADVANTAGE** - The inventive system allows for sharing problem specific objects, algorithms, and analyses among several application programs including a display function, serviced by the server, capable of executing procedures without writing the program codes and properties in the application codes of each client. It provides for a client/server interface in which both the client and the server are implementation language-neutral and architecture-independent. It facilitates dynamic object creation through just in time communication of correct object classes from the server to the client and the client to the server, and facilitates dynamic access by the client to software applications that are resident on the server, thus the invention presents a dual model which allows clients access in the absence of permanently-loaded software to software applications residing on the server. The system is configurable so that if a pharmaceutical company has its own proprietary research database, as well as access to databases licensed from other sources, a database search could automatically search all these public and proprietary databases with a common interface. It solves communication problem and catalyzes collaborations between research groups within the company.

**DESCRIPTION OF DRAWING(S)** - The figure is a client- **view** flowchart for accessing the inventive system.

pp; 34 DwgNo 5a/10  
 Title Terms: RESEARCH; SYSTEM; FACILITATE; DRUG; DISCOVER; DESIGN; COMPRISE  
 ; TWO; COMPUTER; RESPECTIVE; RUN; MULTI; PLATFORM; OBJECT; ORIENT;  
 PROGRAM; CODE; STORAGE; VERTICAL; MARKET; SPECIFIC; DATA; NETWORK;  
 ARCHITECTURE  
 Derwent Class: B04; D16; S03; T01  
 International Patent Class (Main): G06F-013/00; G06F-015/16  
 International Patent Class (Additional): G01N-033/50  
 File Segment: CPI; EPI

6/5/30 (Item 30 from file: 350)  
 DIALOG(R)File 350:Derwent WPIX  
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013760678 \*\*Image available\*\*  
 WPI Acc No: 2001-244890/200125  
 XRAM Acc No: C01-073512  
 XRPX Acc No: N01-174360

Biological data searching and display, used in bioinformatics ,  
 comprises displaying graphical representation of modules which are  
 selected from listing obtained by searching catalog using probe sequence  
 Patent Assignee: ERAGEN BIOSCIENCES INC (ERAG-N)  
 Inventor: BENNER S A; CHAMBERLIN S; KNECHT L  
 Number of Countries: 095 Number of Patents: 005  
 Patent Family:

Patent No	Kind	Date	Applicat No	Kind	Date	Week
WO 200120535	A2	20010322	WO 2000US25247	A	20000914	200125 B
AU 200074881	A	20010417	AU 200074881	A	20000914	200140
EP 1221126	A2	20020710	EP 2000963469	A	20000914	200253
			WO 2000US25247	A	20000914	
JP 2003509776	W	20030311	WO 2000US25247	A	20000914	200319
			JP 2001524043	A	20000914	
CN 1390332	A	20030108	CN 2000815674	A	20000914	200334

Priority Applications (No Type Date): US 99397335 A 19990914; US 99154149 P 19990914

Patent Details:

Patent No	Kind	Lan	Pg	Main IPC	Filing Notes
WO 200120535	A2	E	83	G06F-019/00	
Designated States (National): AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
Designated States (Regional): AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW					
AU 200074881	A			G06F-019/00	Based on patent WO 200120535
EP 1221126	A2	E		G06F-019/00	Based on patent WO 200120535
Designated States (Regional): AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
JP 2003509776	W		80	G06F-017/30	Based on patent WO 200120535
CN 1390332	A			G06F-019/00	

Abstract (Basic): WO 200120535 A2

NOVELTY - Searching a catalog, comprising related biological data using a probe sequence to obtain a search result listing displayed in graphical form showing relationship between the probe and each region of a protein sequence, is new. The required region is selected and a graphical representation of a sequence of various regions along with its amino acid range is displayed.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a computer system for searching and displaying biological data so that patterns in the evolutionary relationships between genomic sequences can be explored, comprising:

(a) input means for selecting at least one catalog comprising an organized body of related biological data;

(b) processing means for searching the catalog using a probe

sequence to obtain a listing of search results displayed in graphical form showing the relationship between the probe sequence and each protein sequence region, that is evolutionarily related to the probe sequence;

(c) input means for selecting a region of interest from the search results listing; and

(d) display means for displaying a family comprising a set of all sequences having the selected region, each sequence of the set includes a graphical representation of the regions of the sequence along its amino acid range;

(2) a graphical user interface for searching and displaying biological data so that patterns in the evolutionary relationships between genomic sequences can be explored, comprising:

(a) a display area for selecting at least one catalog comprising an organized body of related data;

(b) a display area for searching the catalog using a probe sequence;

(c) a display area providing a listing of search results displayed in graphical form which shows the relationship between the probe sequence and each protein sequence region that is related to it;

(d) a display area for displaying a family which comprises a set of all sequences having the selected region, each sequence of the set includes a corresponding graphical representation of the regions of the sequence along its amino acid range;

(3) a graphical user interface for displaying biological data so that patterns in the evolutionary relationships between genomic sequences can be explored, comprising a display area for displaying a family containing a set of all sequences having a selected region of a protein sequence, each sequence in the set including a two-dimensional spatially oriented graphical representation of the various regions of the sequence along its amino acid range;

(4) a computer readable media containing program instructions for displaying data on a display device of a computer system, where the data is obtained from tables in a database associated with the computer system, and comprising:

(a) a computer program code for selecting at least one catalog which contains an organized body of related biological data;

(b) a program code for searching the catalog using a probe sequence to obtain a listing of search results displayed in graphical form showing the relationship between the probe sequence and each region of a protein sequence evolutionarily related to the probe sequence;

(c) computer program code for selecting a region of interest from the search results listing; and

(d) a computer program code for displaying a family comprising a set of all sequences having the selected region;

(5) a computerized storage and retrieval system of biological information comprising a data storage means for storing data in a relational database containing tables, each table has a domain of at least one attribute in common with at least one other table, the tables store all amino acid sequences available in the database, all catalogs available in the database, all annotations of all families, all families of all catalogs, all regions of all catalogs, all profiles of all families, all annotations of all sequences in the database, all types of sequence annotations in the database, all sequence databases available in the database, and all indexed keys of a sequence;

(6) a computer system for storing and retrieving biological data, comprising relational database for storing biological data comprising interrelated tables, each containing an attribute having a common domain with an attribute of at least one other table in the database, and means for viewing patterns in the evolutionary relationships between genomic sequences on the basis of the data stored in the database;

(7) a computer system for storing and retrieving biological data, comprising a database comprising interrelated tables, and means for viewing patterns in the evolutionary relationships between genomic sequences on the basis of stored data; and

(8) graphically representing on a display device information about long distance homology between modules, each comprising a common

subsequence, comprising:

- (a) selecting a module of interest; and
- (b) displaying a set of all proteins in a database possessing the module, each protein in the set having a graphical **view** of its modules, where the selected module and other homologous modules at analogous positions are visually distinguished.

USE - For searching and displaying biological data in **bioinformatics** .

ADVANTAGE - The method allows users to directly use the data returned by one or more queries as the basis for making additional queries. Access to all of the information on a given topic is possible resulting in the discovery of new data connections and relationships. The user is able to more efficiently and effectively review related biological information.

DESCRIPTION OF DRAWING(S) - The drawing shows a navigation flow chart of a method of searching and displaying biological data.

pp; 83 DwgNo 6/20

Title Terms: BIOLOGICAL; DATA; SEARCH; DISPLAY; COMPRISE; DISPLAY;  
GRAPHICAL; REPRESENT; MODULE; SELECT; LIST; OBTAIN; SEARCH; CATALOGUE;  
PROBE; SEQUENCE

Derwent Class: B04; D16; T01

International Patent Class (Main): G06F-017/30; G06F-019/00

International Patent Class (Additional): C12M-001/00

File Segment: CPI; EPI

File 348:EUROPEAN PATENTS 1978-2005/Feb W03

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File 349:PCT FULLTEXT 1979-2002/UB=20050224,UT=20050217

(c) 2005 WIPO/Univentio

Set	Items	Description
S1	3737	BIOLOGICAL(1W)(DATA OR INFORMATION)(1W)MANAG? OR BIOINFORM- ATIC? ? OR BIO()INFORMATIC? ?
S2	1614041	TEMPLATE? ? OR LAYOUT? ? OR FORM? ?
S3	26894	S2(5N)(PREDETERMIN? OR PRESET? OR PREESTABLISH? OR PREDEFI- N? OR PREDESIGNATED OR PREARRANGED OR PRESCRIBED OR (PREVIOUS- LY OR PRE)() (DETERMIN? OR SET???? OR ESTABLISH? OR DEFIN? OR - DESIGNATED OR SCRIBED OR ARRANGED))
S4	10688	(DEFAULT OR FIXED)(3W)S2
S5	1	S1(100N)S3:S4
S6	264	S1(50N)S2
S7	58	S6 AND IC=G06F
S8	42	S7 AND AC=US/PR
S9	30	S8 AND AY=(1970:2001)/PR
S10	10	S7 AND PY=1970:2001
S11	33	S9:S10
S12	4	BIOLOGICAL(1W)(DATA OR INFORMATION)(1W)MANAG?

11/3,K/1 (Item 1 from file: 348)  
DIALOG(R)File 348:EUROPEAN PATENTS  
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01704620

**Method and apparatus for providing a bioinformatics database**  
**Verfahren und Vorrichtung zur Herstellung einer Bio-Informatik-Datenbank**  
**Procede et appareil d'obtention d'une base de donnees bioinformatiques**  
PATENT ASSIGNEE:

Affymetrix, Inc., (2060631), 3380 Central Expressway, Santa Clara, CA  
95051, (US), (Applicant designated States: all)

INVENTOR:

Balaban, David J., 37 Bret Harte Road, San Rafael, CA 94901, (US)  
Aggarwal, Arun, 3374 Tryna Drive, Mountain View, CA 94040, (US)

LEGAL REPRESENTATIVE:

UEXKULL & STOLBERG (100011), Patentanwalte Beselerstrasse 4, 22607  
Hamburg, (DE)

PATENT (CC, No, Kind, Date): EP 1396800 A2 040310 (Basic)

APPLICATION (CC, No, Date): EP 2003025794 980724;

PRIORITY (CC, No, Date): US 53842 P 970725; US 69198 P 971211; US 69436 P  
971211

DESIGNATED STATES: AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LI;  
LU; MC; NL; PT; SE

RELATED PARENT NUMBER(S) - PN (AN):

EP 1002264 (EP 98936012)

INTERNATIONAL PATENT CLASS: G06F-017/30

ABSTRACT WORD COUNT: 71

NOTE:

Figure number on first page: 1

LANGUAGE (Publication,Procedural,Application): English; English; English

FULLTEXT AVAILABILITY:

Available Text	Language	Update	Word Count
CLAIMS A	(English)	200411	964
SPEC A	(English)	200411	7787
Total word count - document A			8751
Total word count - document B			0
Total word count - documents A + B			8751

INTERNATIONAL PATENT CLASS: G06F-017/30

...SPECIFICATION array. Optionally, chip design system 104 may obtain information regarding a specific genetic sequence of interest from **bioinformatics** database 102 or from external databases such as GenBank. The output of chip design system 104 is a set of chip design computer files in the **form** of, for example, a switch matrix, as described in PCT application WO 92/10092, and other associated computer files. The chip design computer files **form** a part of **bioinformatics** database 102. Systems for designing chips for sequence determination and expression analysis are disclosed in U.S...

...related measurements, such as voltage) as a function of position on the substrate. These image files also **form** a part of **bioinformatics** database 102. Since higher photon counts will be observed where the labeled receptor has bound more strongly...

11/3,K/2 (Item 2 from file: 348)  
DIALOG(R)File 348:EUROPEAN PATENTS  
(c) 2005 European Patent Office. All rts. reserv.

01507255

**Database model, tools and methods for organizing information across external information objects**  
**Datenbankmodell, Werkzeuge und Verfahren zum Organisieren von Information unter externen Informationsobjekten**  
**Modele de base de donnees, outils et methode pour organiser des informations parmi des objets informatifs externes**

PATENT ASSIGNEE:

Agilent Technologies Inc, (2885681), 395 Page Mill Road, Palo Alto, CA 94306-2024, (US), (Applicant designated States: all)

INVENTOR:

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MOH, David, 282 Romain Street, San Francisco, CA 94131, (US)  
GRAHAM, Katherine D., 6167 Silberman Drive, San Jose, CA 95120, (US)  
CREECH, Michael L., 1734 Austin Avenue, Los Altos, CA 94024, (US)

LEGAL REPRESENTATIVE:

Schoppe, Fritz, Dipl.-Ing. (55464), Patentanwalte Schoppe, Zimmermann, Stockeler & Zinkler, Postfach 71 08 67, 81458 Munchen, (DE)

PATENT (CC, No, Kind, Date): EP 1260918 A2 021127 (Basic)

APPLICATION (CC, No, Date): EP 2002011256 020522;

PRIORITY (CC, No, Date): US 863115 010522

DESIGNATED STATES: AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LI; LU; MC; NL; PT; SE; TR

EXTENDED DESIGNATED STATES: AL; LT; LV; MK; RO; SI

INTERNATIONAL PATENT CLASS: G06F-017/30

ABSTRACT WORD COUNT: 187

NOTE:

Figure number on first page: 1

LANGUAGE (Publication,Procedural,Application): English; English; English

FULLTEXT AVAILABILITY:

Available Text	Language	Update	Word Count
CLAIMS A	(English)	200248	976
SPEC A	(English)	200248	12276
Total word count - document A			13252
Total word count - document B			0
Total word count - documents A + B			13252

INTERNATIONAL PATENT CLASS: G06F-017/30

...SPECIFICATION across a set of different tumor tissues, contrasting each with gene expression levels for normal tissue. Many **bioinformatics** tools and databases store gene expression data in this **form**, so it is relatively straightforward to import gene expression data into the software. In this example, expression...

11/3,K/3 (Item 3 from file: 348)

DIALOG(R)File 348:EUROPEAN PATENTS

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01453807

**Method for providing clinical diagnostic services**

**Verfahren zum Bereitstellen von klinisch-diagnostischen Diensten**

**Procede permettant de fournir des services de diagnostic clinique**

PATENT ASSIGNEE:

Ortho Clinical Diagnostics Inc., (4077400), 100 Indigo Creek Drive, Rochester, New York 14626, (US), (Applicant designated States: all)

INVENTOR:

Atkins, David, 57 Deforest Avenue, Summit, New Jersey 07901, (US)

LEGAL REPRESENTATIVE:

Mercer, Christopher Paul et al (46611), Carpmiels & Ransford 43, Bloomsbury Square, London WC1A 2RA, (GB)

PATENT (CC, No, Kind, Date): EP 1244047 A2 020925 (Basic)

APPLICATION (CC, No, Date): EP 2002251970 020320;

PRIORITY (CC, No, Date): US 277237 010320

DESIGNATED STATES: AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LI; LU; MC; NL; PT; SE; TR

EXTENDED DESIGNATED STATES: AL; LT; LV; MK; RO; SI

INTERNATIONAL PATENT CLASS: G06F-019/00

ABSTRACT WORD COUNT: 120

NOTE:

Figure number on first page: 1

LANGUAGE (Publication,Procedural,Application): English; English; English



FULLTEXT AVAILABILITY:

Available Text	Language	Update	Word Count
CLAIMS A	(English)	200239	407
SPEC A	(English)	200239	9204
Total word count - document A			9611
Total word count - document B			0
Total word count - documents A + B			9611

INTERNATIONAL PATENT CLASS: G06F-019/00

...SPECIFICATION for rendering data anonymous as each is described infra.

The pattern obtained is provided in any input **form** (e.g., scanned into computer that can digitized the pattern) and then analyzed by the operator of the **bioinformatic** system. The results of the analysis (sequence/pattern match with predicted diagnosis or condition) are then communicated...

11/3,K/5 (Item 5 from file: 348)  
 DIALOG(R)File 348:EUROPEAN PATENTS  
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01026806

METHOD FOR PROVIDING A BIOINFORMATICS DATABASE

VERFAHREN ZUR HERSTELLUNG EINER BIO-INFORMATIK-DATENBANK

PROCEDE D'OBTENTION D'UNE BASE DE DONNEES BIOINFORMATIQUE

PATENT ASSIGNEE:

Affymetrix, Inc. (a Delaware Corporation), (2780470), 3380 Central Expressway, Santa Clara, CA 95051, (US), (Proprietor designated states: all)

INVENTOR:

BALABAN, David, J., 37 Bret Harte Road, San Rafael, CA 94901, (US)

AGGARWAL, Arun, 3374 Tryna Drive, Mountain View, CA 94040, (US)

LEGAL REPRESENTATIVE:

UEXKULL & STOLBERG (100011), Patentanwälte Beselerstrasse 4, 22607 Hamburg, (DE)

PATENT (CC, No, Kind, Date): EP 1002264 A2 000524 (Basic)  
 EP 1002264 B1 040414  
 WO 1999005591 990204

APPLICATION (CC, No, Date): EP 98936012 980724; WO 98US15469 980724

PRIORITY (CC, No, Date): US 53842 P 970725; US 69198 P 971211; US 69436 P 971211

DESIGNATED STATES: AT; BE; CH; CY; DE; DK; ES; FI; FR; GB; GR; IE; IT; LI; LU; MC; NL; PT; SE

RELATED DIVISIONAL NUMBER(S) - PN (AN):

EP 1396800 (EP 2003025794)

INTERNATIONAL PATENT CLASS: G06F-017/30

NOTE:

No A-document published by EPO

LANGUAGE (Publication,Procedural,Application): English; English; English

FULLTEXT AVAILABILITY:

Available Text	Language	Update	Word Count
CLAIMS B	(English)	200416	697
CLAIMS B	(German)	200416	641
CLAIMS B	(French)	200416	832
SPEC B	(English)	200416	7275
Total word count - document A			0
Total word count - document B			9445
Total word count - documents A + B			9445

INTERNATIONAL PATENT CLASS: G06F-017/30

...SPECIFICATION The output of chip design system 104 is a set of chip design computer files in the **form** of, for example, a switch matrix, as described in PCT application WO 92/10092, and other associated computer files. The chip design computer files **form** a part of **bioinformatics** database 102. Systems for designing chips for sequence determination and expression analysis are disclosed in U.S...

...related measurements, such as voltage) as a function of position on the substrate. These image files also form a part of bioinformatics database 102. Since higher photon counts will be observed where the labeled receptor has bound more strongly...

11/3,K/10 (Item 4 from file: 349)  
DIALOG(R)File 349:PCT FULLTEXT  
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00960630 \*\*Image available\*\*

SYSTEM FOR CELLULAR STORAGE AND GENETIC INFORMATION RETRIEVAL  
SYSTEME DE STOCKAGE CELLULAIRE ET DE RECUPERATION D'INFORMATION GENETIQUE  
Patent Applicant/Inventor:

NIETFELD J J, Spechtenkamp 99, NL-3607 KE Maarssen, NL, NL (Residence),  
NL (Nationality)

Legal Representative:

SZYNKA Dirk Konig Szyuka Von Renesse (agent), Sollner Strasse 9, 81479  
Munich, DE,

Patent and Priority Information (Country, Number, Date):

Patent: WO 200294439 A2-A3 20021128 (WO 0294439)

Application: WO 2002IB2271 20020409 (PCT/WO IB0202271)

Priority Application: US 2001282742 20010410

Designated States:

(Protection type is "patent" unless otherwise stated - for applications  
prior to 2004)

AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ  
EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR  
LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL  
TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

(EP) AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR

(OA) BF BJ CF CG CI CM GA GN GQ GW ML MR NE SN TD TG

(AP) GH GM KE LS MW MZ SD SL SZ TZ UG ZM ZW

(EA) AM AZ BY KG KZ MD RU TJ TM

Publication Language: English

Filing Language: English

Fulltext Word Count: 2648

Main International Patent Class: G06F-017/30

Fulltext Availability:

Detailed Description

Detailed Description

... be retrieved and used in various fashions. For example, subscribers to the present system may retrieve the bio - informatic data as anonymous bulk information, as 0 may be desired for medical research. It is contemplated that bio - informatic data may be accessed and retrieved by healthcare professionals, such as on behalf of individuals, to facilitate medical diagnosis and treatment. Use of a biological key, in digital form, will be required for retrieval of up to that point strictly anonymous individual genetic information, thus assuring...  
...contributed to the system.

As noted above, it is contemplated that revenue generated from the supply of bio - informatic data will facilitate storage of the cellular material from which the genetic data is obtained.

11/3,K/12 (Item 6 from file: 349)  
DIALOG(R)File 349:PCT FULLTEXT  
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00940345

A SYSTEM AND METHOD FOR RETRIEVING AND USING GENE EXPRESSION DATA FROM  
MULTIPLE SOURCES  
SYSTEME ET PROCEDE D'EXTRACTION ET D'UTILISATION DE DONNEES D'EXPRESSION

**GENIQUE PROVENANT DE MULTIPLES SOURCES**

Patent Applicant/Assignee:

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(Residence), US (Nationality), (For all designated states except: US)

Patent Applicant/Inventor:

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TOPALOGLOU Thodoros, 657 Middle Avenue, Menlo Park, CA 94025, US, US

(Residence), IL (Nationality), (Designated only for: US)

CHEN Amy, \*\*, (Designated only for: US)

Legal Representative:

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N.W., Suite 900, Washington, DC 20005, US,

Patent and Priority Information (Country, Number, Date):

Patent: WO 200273504 A1 20020919 (WO 0273504)

Application: WO 2002US7727 20020314 (PCT/WO US0207727)

Priority Application: US 2001275465 20010314

Designated States:

(Protection type is "patent" unless otherwise stated - for applications  
prior to 2004)

AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ

EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR

LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI

SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW

(EP) AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR

(OA) BF BJ CF CG CI CM GA GN GQ GW ML MR NE SN TD TG

(AP) GH GM KE LS MW MZ SD SL SZ TZ UG ZM ZW

(EA) AM AZ BY KG KZ MD RU TJ TM

Publication Language: English

Filing Language: English

Fulltext Word Count: 46626

Main International Patent Class: **G06F-019/00**

Fulltext Availability:

Detailed Description

Detailed Description

... changing. An ontology of biological terminology provides a model of  
biological concepts that can be used to **form** a semantic framework for  
many data storage, retrieval, and analysis tasks. Such a semantic  
framework could be used to facilitate seamless integration of various  
heterogeneous **bioinformatics** data, and allows uniform querying across  
them.

Gene Ontology (GO) terms are defined by three different principles...

11/3,K/15 (Item 9 from file: 349)

DIALOG(R)File 349:PCT FULLTEXT

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00921106 \*\*Image available\*\*

**SYSTEM, METHOD, SOFTWARE ARCHITECTURE AND BUSINESS MODEL FOR AN INTELLIGENT  
OBJECT BASED INFORMATION TECHNOLOGY PLATFORM**

**SYSTEME, PROCEDE, ARCHITECTURE LOGICIELLE ET MODELE DE GESTION POUR  
PLATE-FORME DE TECHNOLOGIE D'INFORMATIONS FONDEE SUR UN OBJET  
INTELLIGENT**

Patent Applicant/Assignee:

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Patent and Priority Information (Country, Number, Date):

Patent: WO 200254171 A2-A3 20020711 (WO 0254171)  
Application: WO 2001US47922 20011206 (PCT/WO US0147922)  
Priority Application: US 2000254063 20001206; US 2000254062 20001206; US 2000254064 20001206; US 2000259050 20001229; US 2001246238 20010125; US 2001266957 20010206; US 2001276711 20010316; US 2001282656 20010409; US 2001282658 20010409; US 2001282654 20010409; US 2001282657 20010409; US 2001282655 20010409; US 2001282979 20010410; US 2001282989 20010410; US 2001282991 20010410; US 2001282990 20010410

Designated States:

(Protection type is "patent" unless otherwise stated - for applications prior to 2004)

AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ  
EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR  
LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI  
SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZM ZW  
(EP) AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR  
(OA) BF BJ CF CG CI CM GA GN GQ GW ML MR NE SN TD TG  
(AP) GH GM KE LS MW MZ SD SL SZ TZ UG ZM ZW  
(EA) AM AZ BY KG KZ MD RU TJ TM

Publication Language: English

Filing Language: English

Fulltext Word Count: 78272

Main International Patent Class: G06F-017/30

Fulltext Availability:

Detailed Description

Detailed Description

... data management, and software architecture in the life sciences, biotechnology, therapeutic 5 diagnostic and intervention, pharmaceuticals, and **bioinformatics**, also extendable to other scientific, business and information-oriented application domains.

BACKGROUND

As demand for effective Information...

11/3,K/28 (Item 22 from file: 349)

DIALOG(R)File 349:PCT FULLTEXT

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00822279 \*\*Image available\*\*

INTEGRATED ACCESS TO BIOMEDICAL RESOURCES

ACCES INTEGRE A DES RESSOURCES BIOMEDICALES

Patent Applicant/Assignee:

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ROBERTS Jon L (et al) (agent), Roberts Abokhair and Mardula, LLC, Suite 1000, 11800 Sunrise Valley Drive, Reston, VA 20191, US,

Patent and Priority Information (Country, Number, Date):

Patent: WO 200155911 A1 20010802 (WO 0155911)  
Application: WO 2001US2527 20010126 (PCT/WO US0102527)  
Priority Application: US 2000491920 20000127

Designated States:

(Protection type is "patent" unless otherwise stated - for applications prior to 2004)

DE GB JP

(EP) AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR

Publication Language: English

Filing Language: English

Fulltext Word Count: 6433

Patent and Priority Information (Country, Number, Date):

Patent: ... 20010802

Main International Patent Class: G06F-017/30

Fulltext Availability:

Detailed Description

Publication Year: 2001

Detailed Description

... to interactively access and navigate genomic data files over the Internet, whether those files be in the **form** of HTNIL (as is typically done) or in other formats the data may appear.

SUMMARY OF THE INVENTION

It is an object of the present invention to provide a **bioinformatics** visualization tool that will automatically interpret data from diverse genomic databases (each containing genomic data objects of...

11/3,K/32 (Item 26 from file: 349)

DIALOG(R)File 349:PCT FULLTEXT

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00552847 \*\*Image available\*\*

METHOD AND APPARATUS FOR PROVIDING AN EXPRESSION DATA MINING DATABASE AND LABORATORY INFORMATION MANAGEMENT

DISPOSITIF ET PROCEDURE POUR L'ELABORATION D'UNE BASE DE DONNEES QUI PERMET D'EXTRAIRE DES DONNEES RELATIVES A L'EXPRESSION ET D'ASSURER LA GESTION D'INFORMATIONS DE LABORATOIRE

Patent Applicant/Assignee:

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KHURGIN Elina,  
BERNHART Derek H,  
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AGGARWAL Arun,  
JEVONS Luis,

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JEVONS Luis,

Patent and Priority Information (Country, Number, Date):

Patent: WO 200016220 A1 20000323 (WO 0016220)

Application: WO 99US21305 19990915 (PCT/WO US9921305)

Priority Application: US 98100724 19980917; US 98100740 19980917; US 99354935 19990715

Designated States:

(Protection type is "patent" unless otherwise stated - for applications prior to 2004)

AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES FI GB  
GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD  
MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG  
US UZ VN YU ZA ZW GH GM KE LS MW SD SL SZ TZ UG ZW AM AZ BY KG KZ MD RU  
TJ TM AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE BF BJ CF CG  
CI CM GA GN GW ML MR NE SN TD TG

Publication Language: English

Fulltext Word Count: 25781

Patent and Priority Information (Country, Number, Date):

Patent: ... 20000323

Main International Patent Class: G06F-017/30

Fulltext Availability:

Detailed Description

Publication Year: 2000

Detailed Description

... array. Optionally, chip design system 104 may obtain information regarding a specific genetic sequence of interest from **bioinformatics** database 102 or from external databases such as GenBank. The output of chip design system 104 is a set of chip design computer files in the **form** of, for example, a switch matrix, as described in PCT application WO 92/10092, and other associated...

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	57	(template\$1 or form\$1 or speedsheets\$1) same (biological near2 experiment\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:20
L2	1	(template\$1 or form\$1 or speedsheets\$1) same (biological near2 experiment\$1) same attribute\$1	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:16
L3	1	1 and "707"/\$.ccs.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:17
L4	378	((generat\$3 or creat\$3) near2 (template\$1 or form\$1 or speedsheets\$1)) same experiment\$1	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:21
L5	55	((generat\$3 or creat\$3) near2 (template\$1 or form\$1 or speedsheets\$1)) and (biological near2 experiment\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:31
L6	5	((((generat\$3 or creat\$3) near2 (template\$1 or form\$1 or speedsheets\$1) with library)) and (biological near2 experiment\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:32
L7	8	((((generat\$3 or creat\$3) near2 (template\$1 or form\$1 or speedsheets\$1) with library)) same experiment\$1	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:33
L8	2	((((generat\$3 or creat\$3) near2 (template\$1 or form\$1 or speedsheets\$1) with library)) same experiment\$1	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:33
L9	2	((((generat\$3 or creat\$3) near2 (template\$1 or form\$1 or speedsheets\$1) with library)) same experiment\$1	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:33
L10	558	((generat\$3 or creat\$3) near2 (template\$1 or speedsheets\$1 or form\$1)) same experiment\$1	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:36

L11	378	((generat\$3 or creat\$3) near2 (template\$1 or speadsheet\$1 or form\$1)) same experiment\$1	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:36
L12	3	((generat\$3 or creat\$3) near2 (template\$1 or speadsheet\$1 or form\$1)) same experiment\$1 same attribut\$2	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:37
L13	3	((generat\$3 or creat\$3) near2 (template\$1 or speadsheet\$1 or form\$1)) same experiment\$1 same identifier\$1	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:37
L14	9	((generat\$3 or creat\$3) near2 (template\$1 or speadsheet\$1 or form\$1)) and (experiment\$1 with identifier\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:38
L15	28	((generat\$3 or creat\$3) with (experiment\$1 with identifier\$1))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:41
L16	226	((generat\$3 or creat\$3) with (experiment\$2 near2 (template\$1 or table\$1 or form\$1)))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:00
L17	14	16 and (experiment\$3 near2 attribute\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 12:43
L18	16912	((generat\$3 or creat\$3 or spreadsheet\$1 or table\$1) with (experiment\$2 near2 (template\$1 or table\$1 or form\$1)))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:07
L19	104	18 and (probe near2 array)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:02
L20	83	19 and ((default or library) nea2 template\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:03



L21	260	((generat\$3 or creat\$3) with (experiment\$4 near2 (table\$1 or form\$1 or speadsheet\$1 or template\$1)))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:10
L22	3	((generat\$3 or creat\$3) with (experiment\$4 near2 (table\$1 or form\$1 or speadsheet\$1 or template\$1))) same attribut\$2	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:11
L23	19	21 and (probe near2 array)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:10
L24	3	((generat\$3 or creat\$3) with (experiment\$4 near2 (table\$1 or form\$1 or speadsheet\$1 or template\$1))) same biological	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:16
L25	260	((generat\$3 or creat\$3) with (experiment\$4 near2 (table\$1 or form\$1 or speadsheet\$1 or template\$1)))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:20
L26	56	25 and attribut\$2	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:17
L27	1	((generat\$3 or creat\$3) near2 (table\$1 or form\$1 or speadsheet\$1 or template\$1)) same (biological near2 experiment\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:21
L28	72	((generat\$3 or creat\$3) near2 (table\$1 or form\$1 or speadsheet\$1 or template\$1)) and (biological near2 experiment\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:21
L29	21	((generat\$3 or creat\$3) near2 (table\$1 or form\$1 or speadsheet\$1 or template\$1)) and (biological near2 experiment\$1) and attribut\$2	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:26
L30	226	((generat\$3 or creat\$3) with (experiment\$2 near2 (table\$1 or form\$1 or speadsheet\$1 or template\$1)))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:57

L31	10	30 and "707"/\$.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:27
L32	635	((generat\$3 or creat\$3) with (table\$1 or form\$1 or spreadsheet\$1 or template\$1)) and ((chemical or biological) near2 experiment\$2)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 13:58
L33	10	((generat\$3 or creat\$3) with (table\$1 or form\$1 or spreadsheet\$1 or template\$1) with attribut\$2) and ((chemical or biological) near2 experiment\$2)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 14:47
L34	8	((generat\$3 or creat\$3) near2 (table\$1 or form\$1 or spreadsheet\$1 or template\$1) with attribut\$2) and ((chemical or biological) near2 experiment\$2)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 14:48
L35	1301	((generat\$3 or creat\$3) near2 (table\$1 or form\$1 or spreadsheet\$1 or template\$1) with attribut\$2)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 15:21
L36	1	35 and (experiment\$2 near2 template\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 14:49
L37	382	35 and "707"/\$.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 15:36
L38	88	35 and "707"/3.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 14:49
L39	2551	((generat\$3 or creat\$3) near2 (table\$1 or form\$1 or spreadsheet\$1 or template\$1)) and (defin\$3 near2 attribut\$2)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 15:35
L40	2	((generat\$3 or creat\$3) near2 (experiment\$2 near2 (table\$1 or form\$1 or spreadsheet\$1 or template\$1))) and (defin\$3 near2 attribut\$2)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 15:36

L41	735	39 and "707"/\$.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 15:36
L42	149	39 and "707"/102.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 15:36
L43	3	((generat\$3 or creat\$3) near2 (experiment\$2 near2 (table\$1 or form\$1 or speadsheet\$1 or template\$1))) and "707"/\$.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 15:37
L44	72	((generat\$3 or creat\$3) near2 (table\$1 or form\$1 or speadsheet\$1 or template\$1)) and (biological near2 experiment\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:02
L45	4	44 and "707"/\$.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 15:37
L46	7	(generat\$3 or creat\$3) same (table\$1 or form\$1 or speadsheet\$1 or template\$1) same (biological near2 experiment\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:03
L47	3711	((generat\$3 or creat\$3) same (table\$1 or form\$1 or speadsheet\$1 or template\$1)) and (probe near2 array)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:04
L48	21	47 and "707"/\$.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:04
L49	19	((generat\$3 or creat\$3) with (experiment\$2 near2 (table\$1 or form\$1 or speadsheet\$1 or template\$1))) and (probe near2 array)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:10
L50	25	((generat\$3 or creat\$3) with (table\$1 or form\$1 or speadsheet\$1 or template\$1)) and (probe near2 array) and (experiment\$2 near2 template\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:24

L51	0	((generat\$3 or creat\$3) with (table\$1 or form\$1 or spreadsheet\$1 or template\$1)) and (probe near2 array) and (biological near2 experiment\$2)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:11
L52	0	((generat\$3 or creat\$3) with (table\$1 or form\$1 or spreadsheet\$1 or template\$1)) and (probe near2 array) and (biological near2 experiment\$2)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:11
L53	0	(probe near2 array)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:18
L54	7091	(probe near2 array)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:18
L55	4	(probe near2 array) same (biological near2 experiment\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:20
L56	4	(probe near2 array) same ((biological or chemical\$1) near2 experiment\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:20
L57	2777	((generat\$3 or creat\$3) with (table\$1 or form\$1 or spreadsheet\$1 or template\$1)) and ((probe near2 array) or genechip or (spotted near2 array))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:25
L58	21	((generat\$3 or creat\$3) with (experiment\$2 near2 (table\$1 or form\$1 or spreadsheet\$1 or template\$1))) and ((probe near2 array) or genechip or (spotted near2 array))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:27
L59	31	((generat\$3 or creat\$3) same (experiment\$2 near2 (table\$1 or form\$1 or spreadsheet\$1 or template\$1))) and ((probe near2 array) or genechip or (spotted near2 array))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:31
L60	3176	((generat\$3 or creat\$3) same (table\$1 or form\$1 or spreadsheet\$1 or template\$1)) and ((probe near2 array) or genechip or (spotted near2 array)) and biological	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/03/03 16:31

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	3	(template\$1 same (biological near2 experiment\$1))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/02/11 12:19
L2	18648	(experiment\$2 near2 (template\$1 or spreadsheet\$1 or form\$1 or table\$1))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/02/11 12:21
L3	0	2 and ((user near2 selet\$4) near2 templat\$2)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/02/11 12:24
L4	0	2 and (user near2 selet\$4)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/02/11 12:23
L5	147	2 and ((default\$1 or sample\$1) near2 template\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/02/11 12:25
L6	1	5 and (select\$3 with user\$1 with template\$1)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	OR	OFF	2005/02/11 12:25